



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/786,635B  
Source: JFW/b  
Date Processed by STIC: 9/20/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04



IFW16

## RAW SEQUENCE LISTING

DATE: 09/20/2004

PATENT APPLICATION: US/09/786,635B

TIME: 16:18:10

Input Set : A:\LEA33298 - seq list 8-2004.txt

Output Set: N:\CRF4\09202004\I786635B.raw

3 <110> APPLICANT: Bayer AG  
 5 <120> TITLE OF INVENTION: ATP binding cassette genes and proteins for diagnosis  
 6 and treatment of lipid disorders and inflammatory  
 7 diseases  
 9 <130> FILE REFERENCE: ATP binding cassette genes and protein  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/786,635B  
 C--> 12 <141> CURRENT FILING DATE: 2001-05-22  
 14 <150> PRIOR APPLICATION NUMBER: 101706  
 15 <151> PRIOR FILING DATE: 1998-09-25  
 17 <160> NUMBER OF SEQ ID NOS: 54  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 6880  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Human  
 26 <220> FEATURE:  
 27 <223> OTHER INFORMATION: cDNA of ABCA1 (ABC1)  
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 32 atgcccctcg caggaacact tccttgggtt caggggatta tctgtaatgc caacaacccc 180  
 33 tgtttccgtt acccgactcc tggggaggct cccggagttt ttggaaactt taacaaatcc 240  
 34 attgtggctc gcctgttctc agatgctcgg aggcttcttt tatacagcca gaaagacacc 300  
 35 agcatgaagg acatgcgcaa agttctgaga acattacagc agatcaagaa atccagctca 360  
 36 aacttgaagc ttcaagattt cctgggtggac aatgaaacct tctctgggtt cctgtatcac 420  
 37 aacctctctc tcccaaagtc tactgtggac aagatgctga gggctgatgt cattctccac 480  
 38 aaggtattt tgcaaggcta ccagttacat ttgacaagtc tgcataatgg atcaaaatca 540  
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 40 aaactggctg cagcagagcg agtacttcgt tccaacatgg acatcctgaa gccaatcctg 660  
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 42 ttgctgcata gtcttggac tctggcccag gagctgttca gcatgagaag ctggagtgac 780  
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 48 gggaaagatcc tgtatcaccc tgacactcca gccacaaggc aggtcatggc tgaggtgaac 1140  
 49 aagaccttcc aggaactggc tgcgttccat gatctggaaag gcatgtggga ggaactcagc 1200  
 50 cccaaagatct ggaccttcat ggagaacagc caagaaatgg accttgcggc gatgctgtt 1260  
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 54 ttcatggagt gtgtcaaccta gaacaagcta gaacccatag caacagaagt ctggctcatc 1500

MP 5-6  
 Does Not Comply  
 Corrected Diskette Needed

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55 aacaagtcca tggagctgct ggatgagagg aagttctggg ctggattgt gttcactgga 1560  
 56 attactccag gcagcattga gctgccccat catgtcaagt acaagatccg aatggacatt 1620  
 57 gacaatgtgg agaggacaaa taaaatcaag gatgggtact gggaccctgg tcctcgagct 1680  
 58 gaccctttg aggacatgcg gtacgtctgg gggggcttcg cctacttgca ggtatgtgg 1740  
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 60 cagatgccct atccctgtta cgttgatgac atcttctgc gggtcatgag ccggtaatg 1860  
 61 ccccttca tgacgctggc ctggattac tcagtgcgt tgatcatcaa gggcatcg 1920  
 62 tatgagaagg aggcacggct gaaagagacc atgcggatca tggcctgga caacagcatc 1980  
 63 ctctggttta gctggttcat tagtagcctc attcctcttc ttgtgagcgc tggcctgcta 2040  
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 65 ttctgtccg tgggtgtgt ggtgacaatc ctgcagtgc tcctgattag cacactcttc 2160  
 66 tccagagcca acctggcagc agcctgtggg ggcacatct acttcacgct gtacctgccc 2220  
 67 tacgtctgt gtgtggcatg gcaggactac gtgggcttca cactcaagat cttcgctagc 2280  
 68 ctgctgtcc tgggtgttt tgggtttggc tggatgtact ttgccttt tgaggagcag 2340  
 69 ggcattggag tgcagtggga caacctgttt gagagtctg tggaggaaga tggcttaat 2400  
 70 ctaccactt cggctccat gatgctgtt gacacccctt tctatgggt gatgactgg 2460  
 71 tacattgagg ctgtcttcc aggccagttac ggaatttcca ggcctggta tttccttgc 2520  
 72 accaagtcc actgggttgg cgaggaaatg gatgagaaga gccaccctgg ttccaaccag 2580  
 73 aagagaatat cagaatctg catggaggag gaaacccaccc acttgaagct gggcgtgtcc 2640  
 74 attcagaacc tggtaaaatg ctaccgagat gggatgaagg tggctgtcga tggcctggca 2700  
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 76 accaccatgt caatcctgac cgggttgc ccccccaccc cgggcaccgc ctacatctg 2820  
 77 ggaaaagaca ttgccttga gatgagcacc atccggcaga acctgggggt ctgtccccag 2880  
 78 cataacgtgc tgggtgacat gctgactgtc gaagaacaca tctgggtcta tgccctttg 2940  
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 80 ttgccttcaaa gcaagctgaa aagcaaaaca agccagctgt caggtggaaat gcaagagaaag 3060  
 81 ctatctgtgg cttggcctt tgggggggat tctaagggtt tcattcttgc tgaacccaca 3120  
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 83 ggcgcacca ttattcttc tacacaccac atggatgaag cgcacgtcc gggggacagg 3240  
 84 attgccttca tctccatgg gaagctgtgc tgggtggct cttccctgtt tctgaagaac 3300  
 85 cagctggaa caggctacta cctgacccat gtcagaaggat atgtggatc cttccctcagt 3360  
 86 tcctgcagaa acagtagtag cactgtgtca tacctgaaaa aggaggacag tggatgttc 3420  
 87 agcagttctg atgctggcct gggcagcgc catgagatgt acacgctgac catcgatgtc 3480  
 88 tctgttatct ccaacccat caggaagcat gtgtctgaa cccggctgg ggaagacata 3540  
 89 gggcatgagc tgacctatgt gctgccatat gaagctgcta aggaggagc ctttggaa 3600  
 90 ctcttcatg agattgtatg cccgctctca gacctggca tttctatgtt tggcatctca 3660  
 91 gagacgaccc tggaaagaaat attcctcaag gtggccaaag agatgggggt ggtatgtgag 3720  
 92 acctcagatg gtaccttgcg agcaagacga aacaggcgcc cttccggggca aacgcacac 3780  
 93 tgcgtctgc cgttcaactg agatgtatgt gctgatccaa atgattctga catagaccca 3840  
 94 gaatccagag agacagactt gctcagtggg atggatggca aagggtctca ccaggtaaa 3900  
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 97 gcccctgtgt tcaacgttgc cgtgcccacc tttggcaactt accccagcctt ggaacttc 4080  
 98 ccctggatgt acaacgaaca gtacacattt gtcagcaatg atgctcttgc ggacacggg 4140  
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 100 ggaaacccaa tccctggccac gcccctggccag gcaggggagg aagatggac cactgcccc 4260  
 101 gttccccaga ccatcatggc cctcttccat aatggaaact ggacaaatgca gaacccttca 4320  
 102 cctgcacatgc agtgcgttgc cgcacaaaatc aagaagatgc tgcgtctgc tcccccagg 4380  
 103 gcaggggggc tgccttccatcc acaaaagaaaa caaaacactg cagatatctt tcaggacctg 4440

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156	1	5	10	15												
158	Ala	Asn	Asn	Pro	Cys	Phe	Arg	Tyr	Pro	Thr	Pro	Gly	Ala	Pro	Gly	
159															30	
161	Val	Val	Gly	Asn	Phe	Asn	Lys	Ser	Ile	Val	Ala	Arg	Leu	Phe	Ser	Asp
162															45	
164	Ala	Arg	Arg	Leu	Leu	Leu	Tyr	Ser	Gln	Lys	Asp	Thr	Ser	Met	Lys	Asp
165															60	
167	Met	Arg	Lys	Val	Leu	Arg	Thr	Leu	Gln	Gln	Ile	Lys	Lys	Ser	Ser	Ser
168															80	
170	Asn	Leu	Lys	Leu	Gln	Asp	Phe	Leu	Val	Asp	Asn	Glu	Thr	Phe	Ser	Gly
171															95	
173	Phe	Leu	Tyr	His	Asn	Leu	Ser	Leu	Pro	Lys	Ser	Thr	Val	Asp	Lys	Met
174															110	
176	Leu	Arg	Ala	Asp	Val	Ile	Leu	His	Lys	Val	Phe	Leu	Gln	Gly	Tyr	Gln
177															125	
179	Leu	His	Leu	Thr	Ser	Leu	Cys	Asn	Gly	Ser	Lys	Ser	Glu	Glu	Met	Ile
180															140	
182	Gln	Leu	Gly	Asp	Gln	Glu	Val	Ser	Glu	Leu	Cys	Gly	Leu	Pro	Arg	Glu
183															160	
185	Lys	Leu	Ala	Ala	Ala	Glu	Arg	Val	Leu	Arg	Ser	Asn	Met	Asp	Ile	Leu
186															175	
188	Lys	Pro	Ile	Leu	Arg	Thr	Leu	Asn	Ser	Thr	Ser	Pro	Phe	Pro	Ser	Lys
189															190	
191	Glu	Leu	Ala	Glu	Ala	Thr	Lys	Thr	Leu	Leu	His	Ser	Leu	Gly	Thr	Leu
192															205	
194	Ala	Gln	Glu	Leu	Phe	Ser	Met	Arg	Ser	Trp	Ser	Asp	Met	Arg	Gln	Glu
195															220	
197	Val	Met	Phe	Leu	Thr	Asn	Val	Asn	Ser	Ser	Ser	Ser	Ser	Thr	Gln	Ile
198															240	
200	Tyr	Gln	Ala	Val	Ser	Arg	Ile	Val	Cys	Gly	His	Pro	Glu	Gly	Gly	Gly
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203	Leu	Lys	Ile	Lys	Ser	Leu	Asn	Trp	Tyr	Glu	Asp	Asn	Asn	Tyr	Lys	Ala
204															270	
206	Leu	Phe	Gly	Gly	Asn	Gly	Thr	Glu	Glu	Asp	Ala	Glu	Thr	Phe	Tyr	Asp
207															285	
209	Asn	Ser	Thr	Thr	Pro	Tyr	Cys	Asn	Asp	Leu	Met	Lys	Asn	Leu	Glu	Ser
210															300	
212	Ser	Pro	Leu	Ser	Arg	Ile	Ile	Trp	Lys	Ala	Leu	Lys	Pro	Leu	Leu	Val
213															320	
215	Gly	Lys	Ile	Leu	Tyr	Thr	Pro	Asp	Thr	Pro	Ala	Thr	Arg	Gln	Val	Met
216															335	
218	Ala	Glu	Val	Asn	Lys	Thr	Phe	Gln	Glu	Leu	Ala	Val	Phe	His	Asp	Leu
219															350	
221	Glu	Gly	Met	Trp	Glu	Glu	Leu	Ser	Pro	Lys	Ile	Trp	Thr	Phe	Met	Glu
222															365	
224	Asn	Ser	Gln	Glu	Met	Asp	Leu	Val	Arg	Met	Leu	Leu	Asp	Ser	Arg	Asp
225															380	
227	Asn	Asp	His	Phe	Trp	Glu	Gln	Gln	Leu	Asp	Gly	Leu	Asp	Trp	Thr	Ala
228															400	
															395	
															385	

RAW SEQUENCE LISTING  
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Output Set: N:\CRF4\09202004\I786635B.raw

230 Gln Asp Ile Val Ala Phe Leu Ala Lys His Pro Glu Asp Val Gln Ser  
 231 405 410 415  
 233 Ser Asn Gly Ser Val Tyr Thr Trp Arg Glu Ala Phe Asn Glu Thr Asn  
 234 420 425 430  
 236 Gln Ala Ile Arg Thr Ile Ser Arg Phe Met Glu Cys Val Asn Leu Asn  
 237 435 440 445  
 239 Lys Leu Glu Pro Ile Ala Thr Glu Val Trp Leu Ile Asn Lys Ser Met  
 240 450 455 460  
 242 Glu Leu Leu Asp Glu Arg Lys Phe Trp Ala Gly Ile Val Phe Thr Gly  
 243 465 470 475 480  
 245 Ile Thr Pro Gly Ser Ile Glu Leu Pro His His Val Lys Tyr Lys Ile  
 246 485 490 495  
 248 Arg Met Asp Ile Asp Asn Val Glu Arg Thr Asn Lys Ile Lys Asp Gly  
 249 500 505 510  
 251 Tyr Trp Asp Pro Gly Pro Arg Ala Asp Pro Phe Glu Asp Met Arg Tyr  
 252 515 520 525  
 254 Val Trp Gly Gly Phe Ala Tyr Leu Gln Asp Val Val Glu Gln Ala Ile  
 255 530 535 540  
 257 Ile Arg Val Leu Thr Gly Thr Glu Lys Lys Thr Gly Val Tyr Met Gln  
 258 545 550 555 560  
 260 Gln Met Pro Tyr Pro Cys Tyr Val Asp Asp Ile Phe Leu Arg Val Met  
 261 565 570 575  
 263 Ser Arg Ser Met Pro Leu Phe Met Thr Leu Ala Trp Ile Tyr Ser Val  
 264 580 585 590  
 266 Ala Val Ile Ile Lys Gly Ile Val Tyr Glu Lys Glu Ala Arg Leu Lys  
 267 595 600 605  
 269 Glu Thr Met Arg Ile Met Gly Leu Asp Asn Ser Ile Leu Trp Phe Ser  
 270 610 615 620  
 272 Trp Phe Ile Ser Ser Leu Ile Pro Leu Leu Val Ser Ala Gly Leu Leu  
 273 625 630 635 640  
 275 Val Val Ile Leu Lys Leu Gly Asn Leu Leu Pro Tyr Ser Asp Pro Ser  
 276 645 650 655  
 278 Val Val Phe Val Phe Leu Ser Val Phe Ala Val Val Thr Ile Leu Gln  
 279 660 665 670  
 281 Cys Phe Leu Ile Ser Thr Leu Phe Ser Arg Ala Asn Leu Ala Ala Ala  
 282 675 680 685  
 284 Cys Gly Gly Ile Ile Tyr Phe Thr Leu Tyr Leu Pro Tyr Val Leu Cys  
 285 690 695 700  
 287 Val Ala Trp Gln Asp Tyr Val Gly Phe Thr Leu Lys Ile Phe Ala Ser  
 288 705 710 715 720  
 290 Leu Leu Ser Pro Val Ala Phe Gly Phe Gly Cys Glu Tyr Phe Ala Leu  
 291 725 730 735  
 293 Phe Glu Glu Gln Gly Ile Gly Val Gln Trp Asp Asn Leu Phe Glu Ser  
 294 740 745 750  
 296 Pro Val Glu Glu Asp Gly Phe Asn Leu Thr Thr Ser Val Ser Met Met  
 297 755 760 765  
 299 Leu Phe Asp Thr Phe Leu Tyr Gly Val Met Thr Trp Tyr Ile Glu Ala  
 300 770 775 780  
 302 Val Phe Pro Gly Gln Tyr Gly Ile Pro Arg Pro Trp Tyr Phe Pro Cys

09/786, 635B 6

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<211> 1130  
<212> DNA  
<213> Human

<220>  
<223> human cDNA of ABCB9

<400> 3  
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ggaac~~cc~~ccca agtc~~c~~tc~~c~~atc ctggat~~g~~aa~~g~~ ccacc~~g~~gc~~c~~ tttggat~~g~~cc gagag~~g~~g~~a~~ 180  
atctgat~~c~~ca~~g~~ c~~g~~aggccatc catggcaacc t~~g~~t~~c~~aga~~a~~gc acac~~g~~tact catcat~~c~~cg~~g~~ 240  
cacc~~g~~ct~~g~~ga~~c~~ g~~c~~acc~~g~~tg~~g~~ga~~c~~ g~~c~~ac~~g~~gc~~c~~ac~~t~~ c~~t~~catt~~g~~tg~~g~~ tgctggac~~aa~~ gggcc~~g~~cg~~t~~ 300  
gtgc~~g~~agg~~g~~ g~~c~~acc~~g~~ac~~ca~~ g~~c~~ag~~c~~tt~~g~~ct~~t~~ tgcccc~~g~~agg~~g~~ c~~g~~gg~~c~~tt~~t~~ta~~c~~ c~~g~~gca~~a~~g~~c~~th~~g~~ 360  
gttgc~~g~~agg~~g~~ c~~g~~at~~t~~gt~~g~~gg~~g~~ g~~t~~ttca~~g~~agg~~c~~ c~~g~~c~~a~~g~~a~~ct~~t~~c acag~~t~~gg~~g~~cc acaac~~g~~ag~~g~~cc 420  
tgtagcc~~a~~ac~~g~~ ggg~~t~~caca~~g~~ g~~c~~ct~~t~~gat~~g~~gg~~g~~ gggccc~~t~~c~~c~~ ttc~~g~~ccc~~g~~gt~~g~~ g~~c~~aga~~g~~gg~~g~~ac 480  
cc~~g~~gt~~g~~c~~c~~ct~~g~~ c~~c~~t~~g~~g~~c~~ag~~g~~at~~g~~ gt~~g~~cc~~c~~ac~~g~~g ag~~t~~tt~~c~~ca~~g~~ ct~~g~~cc~~c~~t~~a~~cc~~g~~ g~~a~~g~~c~~cc~~g~~gg~~g~~ 540  
ct~~g~~cg~~c~~act~~t~~ gaaag~~a~~gac~~g~~ac~~t~~ ct~~g~~cc~~a~~t~~g~~tc~~t~~ c~~c~~at~~g~~at~~c~~ac~~t~~ c~~g~~c~~t~~tt~~g~~ca~~t~~ at~~t~~tt~~g~~cccc~~t~~ 600  
t~~g~~gt~~g~~cc~~c~~tc~~g~~ cccatt~~cc~~ca~~g~~ ggg~~c~~act~~t~~t~~c~~ acc~~c~~nn~~n~~ct~~t~~ ggg~~g~~at~~g~~tc~~t~~ caa~~g~~ag~~g~~cata~~t~~ 660  
gt~~g~~ct~~c~~t~~c~~cc~~t~~ cata~~cc~~c~~c~~tc~~t~~ c~~a~~g~~a~~ag~~g~~gg~~g~~ g~~c~~tt~~c~~cc~~t~~gt~~g~~ cc~~g~~gagg~~g~~g~~g~~ ac~~a~~c~~g~~gg~~g~~aa~~t~~ 720  
c~~g~~gg~~g~~att~~t~~tc~~t~~ c~~g~~t~~c~~t~~c~~cc~~t~~ t~~c~~t~~t~~g~~c~~cc~~g~~ t~~c~~t~~t~~g~~a~~gt~~g~~ tc~~g~~cc~~c~~agg~~g~~ g~~g~~gt~~g~~agg~~g~~g~~g~~ 780  
c~~g~~t~~g~~agg~~g~~g~~g~~ ac~~t~~t~~g~~t~~c~~tc~~t~~ ca~~t~~tt~~g~~cc~~c~~g~~g~~ ct~~g~~cc~~a~~at~~t~~ a~~a~~g~~c~~ca~~g~~t~~t~~ c~~a~~c~~t~~gt~~g~~acc~~t~~ 840  
ac~~a~~c~~g~~aa~~a~~cc~~t~~ t~~c~~a~~a~~ct~~g~~gg~~g~~ g~~a~~gt~~g~~agg~~g~~ ct~~g~~gg~~c~~cc~~g~~agg~~g~~ ct~~g~~c~~a~~gg~~g~~tg~~g~~cc~~t~~ 900  
ccc~~g~~ag~~g~~cc~~g~~g~~g~~ c~~a~~ccc~~g~~act~~t~~ t~~c~~g~~c~~cc~~c~~tc~~t~~ t~~c~~ca~~a~~t~~c~~acc~~t~~ c~~c~~t~~g~~gg~~g~~ct~~g~~cc~~t~~ ag~~c~~cc~~g~~cc~~c~~ct~~t~~ 960  
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ct~~c~~t~~t~~t~~g~~tc~~t~~ t~~t~~tt~~g~~gt~~g~~ga~~t~~ g~~g~~gat~~g~~gt~~g~~tc~~t~~ aa~~a~~g~~c~~cc~~a~~g~~g~~ at~~t~~tt~~g~~g~~c~~tt~~t~~ g~~c~~c~~a~~g~~g~~gt~~g~~t~~t~~ 1080  
g~~c~~aa~~a~~cat~~g~~tt~~t~~ g~~g~~aga~~a~~cc~~c~~ g~~g~~t~~c~~aa~~t~~aa~~t~~ g~~t~~t~~a~~ct~~a~~cc~~t~~ t~~c~~tt~~a~~cc~~c~~ct~~t~~ 1130

see p. 7  
for error  
Explanation

(h's need  
Explanation  
in 12207-12237  
section)

(g's)

The types of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

VARIABLE LOCATION SUMMARY  
PATENT APPLICATION: US/09/786,635B

DATE: 09/20/2004  
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Input Set : A:\LEA33298 - seq list 8-2004.txt  
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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:3; N Pos. 8,109,360,586,636,637,638,1040

Seq#:4; N Pos. 944,950,957,970,1001,1002,1003,1007

Seq#:13; N Pos. 4208,4210,4211,4212,4227,4228,4229,4231,4253,4677,4691,4707

Seq#:13; N Pos. 4721,4752,4754,4772,4773

Seq#:20; N Pos. 5,2909

Seq#:25; N Pos. 1963

Seq#:31; N Pos. 856,1009,1128,1314,1326,1328,1343,1345,1346,1378,1415,2477

Seq#:31; N Pos. 2540

Seq#:54; N Pos. 856,1009,1128,1314,1326,1328,1343,1345,1346,1378,1415,2477

Seq#:54; N Pos. 2540

**VERIFICATION SUMMARY**

DATE: 09/20/2004

PATENT APPLICATION: US/09/786,635B

TIME: 16:18:11

Input Set : A:\LEA33298 - seq list 8-2004.txt

Output Set: N:\CRF4\09202004\I786635B.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:579 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3  
L:579 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3  
L:579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
M:341 Repeated in SeqNo=3  
L:623 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4  
L:623 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4  
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:900  
M:341 Repeated in SeqNo=4  
L:1205 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13  
L:1205 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13  
L:1205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:4200  
M:341 Repeated in SeqNo=13  
L:1577 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:20  
L:1577 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:20  
L:1577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0  
M:341 Repeated in SeqNo=20  
L:1720 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:25  
L:1720 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:25  
L:1720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:1920  
L:1986 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:31  
L:1986 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:31  
L:1986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:840  
M:341 Repeated in SeqNo=31  
L:2289 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:54  
L:2289 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:54  
L:2289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:840  
M:341 Repeated in SeqNo=54